GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 8, 2003, 16:28:28 ; Search time 343.211 Seconds
                                          (without alignments)
                                          3964.081 Million cell updates/sec

Title: US-10-001-848-3
Perfect score: 2709
Sequence: 1 MTPSPLLLLLPPLLLGAFP.........HSHTHSHVBGKVHQHIHYQC 504

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext 0.5
               Ygapop 10.0 , Ygapext 0.5
               Fgapop   6.0 , Fgapext 7.0
               Delop   6.0 , Delext   7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10001848/runat_08102003_130420_22043/app_query.fasta_1.1166
-DB=N Geneseq_19Jun03 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=bct -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10001848 @CGN_1_1_511 @runat 08102003 130420 22043 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_19Jun03:*
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     3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
     4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
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    23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
    24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
    25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2709	100.0	1512	22	AAF27782	Human MANGO 003 co
2	2709	100.0	3169	22	AAF27781	Human MANGO 003 co
3	2709	100.0	3402	21	AAC58376	Human PRO943 nucle
4	2709	100.0	3402	21	AA264984	Membrane-bound pro
5	2709	100.0	3402	22	AAF44130	Human PRO943 (UNQ4
6	2709	100.0	3402	24	ABK11750	cDNA encoding huma
7	2709	100.0	3402	24	ABK28591	Human DNA52192-136
8	2709	100.0	3402	25	ABX80198	Human secreted or
9	2709	100.0	3402	25	ABX80702	Human secreted/tra
10	2709	100.0	3402	25	ABX81085	Human secreted or
11	2709	100.0	3402	25	ABX90175	Human secreted/tra
12	2709	100.0	3402	25	ABX77786	Human PRO polynucl
13	2709	100.0	3402	25	ABX79382	Human secreted/tr
14	2709	100.0	3402	25	ABX64021	cDNA encoding huma
15	2709	100.0	3402	25	ABX16985	Human PRO polynucl
16	2701	99.7	3101	24	ABQ78867	Human fibroblast g
17	2694	99.4	3112	21	AAA28842	Human fibroblast g
18	2694	99.4	3138	25	ABX34717	Human mddt cDNA SE
19	2516	92.9	1450	23	AAS14936	DNA encoding human
20	2468.5	91.1	3186	25	AAI57799	Human polynucleoti
21	2357	87.0	1967	22	AAA96724	Polynucleotide iso
22	2357	87.0	2274	24	ABQ78868	Mouse fibroblast g
23	2357	87.0	2277	23	AAS14935	DNA encoding murin
24	2095	77.3	2178	22	AAH76216	Human kinase PKIN-
25	1947	71.9	24173	24	ABQ78869	Mouse fibroblast g
26	1877	69.3	1177	22	AAH99452	Human protein enco
27	1877	69.3	1742	21	AAI59585	Human polynucleoti
28	1822	67.3	1742	21	AAA96725	Polynucleotide iso
29	1821	67.2	1788	23	AAS14939	DNA encoding murin
30	1755	64.8	2556	24	ABQ54233	Human ovarian anti
31	1755	64.8	2569	21	AAF16334	Human prostate can
32	1650	60.9	1004	22	AAA96726	Homologue of a pol
33	1496.5	55.2	1423	21	AAA96739	Polynucleotide iso
34	882	32.6	624	22	AAF27784	Murine MANGO 003 c
35	882	32.6	1074	22	AAF27783	Murine MANGO 003 c
36	861	31.8	493	24	ABA90317	Human ORF124 codin
37	831	30.7	854	22	AAH05404	Human cDNA clone (
38	831	30.7	1999	22	AAH18836	Human cDNA sequenc
39	660	24.4	384	21	AAA96723	Polynucleotide iso
40	509	18.8	2409	24	ABZ35764	Human FGFR4 polynu
41	509	18.8	2409	24	ABX10007	Human FGFR4 DNA fr
42	509	18.8	2409	24	ABV78188	Human FGFR4 DNA SE
43	509	18.8	2409	24	ABL91729	Human polynucleoti
44	509	18.8	3015	24	ABV94047	Breast carcinoma r
45	496.5	18.3	8083	23	AAD34802	Mouse fibroblast g

ALIGNMENTS

RESULT 1
AAF27782
ID   AAF27782 standard; cDNA; 1512 BP.
XX
AC   AAF27782;
XX
DT   05-APR-2001 (first entry)
XX
DE   Human MANGO 003 coding sequence SBQ ID NO: 6.
XX
KW   Membrane associated protein; secreted protein; human; mouse; rat;
KW   INTERCEPT 340; MANGO 003; MANGO 347; TANGO 272; TANGO 295; TANGO 354;
KW   TANGO 378; skeletal disorder; cardiovascular disorder; renal disorder;
KW   haematopoietic disorder; neural disorder; hepatic disorder;
KW   neoplastic disease; ss.
XX
OS   Homo sapiens.

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

XX
PN   WO200100673-A1.
XX
PD   04-JAN-2001.
XX
PF   29-JUN-2000; 2000WO-US18198.
XX
PR   30-JUN-1999; 99US-0345464.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
PI   Barnes TM, Fraser CC, Wrighton N, Myers P, Busfield SJ, Sharp JD;
XX
DR   WPI; 2001-050128/06.
XX
PT   Isolated secreted or transmembrane proteins are used for diagnosis and
PT   treatment of neoplastic and haematopoietic disorders e.g. T cell
PT   disorders, cancer and tumours -
XX
PS   Claim 1; Page 217-218; 294pp; English.
XX
CC   The present invention provides the protein and coding sequences for a
CC   number of membrane associated and secreted proteins from human, mouse and
CC   rat. The proteins are designated INTERCEPT 340, MANGO 003, MANGO 347,
CC   TANGO 272, TANGO 295, TANGO 254 and TANGO 378. The proteins are all
CC   involved in signal transduction and the sequences can be used in the
CC   treatment of cardiovascular, renal, hepatic, neural, neoplastic, skeletal
CC   and haematopoietic disorders.
XX
SQ   Sequence 1512 BP; 270 A; 542 C; 480 G; 220 T; 0 other;

Alignment Scores:
Pred. No.:
Score: 1.99e-128
                        2709.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB:

Length: 1512
Matches: 504
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 22

US-10-001-848-3 (1-504) x AAF27782 (1-1512)

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Qy    1 MetThrProSerProLeuLeuLeuLeuProProLeuLeuGlyAlaPhePro       20
Db    1 ATGACGCCGAGCCCCCTTGTGCTCCTGCTGCCGCCGTTGCTGGGGGCCTTCCCG      60

Qy   21 ProAlaAlaAlaArgLysGlyProProLysMetAlaAspAlaLysValProArgGlnVal   40
Db   61 CCGGCCGCCGCCGCCCGAGCCCCCAAAGATGGCGGACAAAGGTGGTCCCACGGCCAGGTG  120

Qy   41 AlaArgLeuGlyArgThrValArgLeuGlnCysCysProValGluGlyValGlyAspProProLeu  60
Db  121 GCCCGGCTGGGCCGCACTGTGCGCCTGCAGTGCCCAGTGGAGGGGGACCCCCGCCCGCTG  180

Qy   61 ThrMetTrpThrLysAspGlyArgThrIleHisSerGlyTrpSerGlyPheArgValLeu   80
Db  181 ACCATGTGGACCAAGGATGGCCGCACCATCCACAGCGGCTGGAGCCGCTTCCGCGTGCTG  240

Qy   81 ProGlnGlyLeuLysValSerGlnValGluArgGluAspAlaGlyValTyrValCysLys  100
Db  241 CCGCAGGGGCTGAAGGTGAGCCAGGTGGAGCGGGAGGATGCCGGCGTGTACGTGTGCAAG  300

Qy  101 AlaThrAsnGlyPheGlySerLeuSerValAsnTyrThrLeuValValLeuAspAspIle  120
Db  301 GCCACCAACGGCTTCGGCAGCCTCAGCGTCAACTACACACCCTCCGTCGTGCTGGATGACATT  360

Qy  121 SerProGlyLysGluSerLeuGlyProAspSerSerGlyGlnGlnAspGluGluProAla  140
Db  361 AGCCCAGGGAAGGAGAGCCTGGGGCCCGACAGCTCCTGGGGGTCAAGACGAGGACCCCGCC  420

Qy  141 SerGlnGlnTrpAlaArgProArgPheThrGlnProSerArgArgProArgValIle  160
Db  421 AGCCAGCAGTGGGCACGACGCCGCTTCACACAGCCCTCCACAGCGCCCTCCAAGATGATGAGGCCGCGGGTGATC  480
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Qy  161 AlaArgProValGlySerSerValArgLeuCysValAlaSerGlyHisProArgPro  180
Db  481 GCACGGCCCGTGGGTAGCTCCGTGCGCCTGTGCGTGGCCAGCGGGCACCCTCGGCCC  540

Qy  181 AspIleThrTrpMetLysAspAspAspGlnAlaLeuThrArgProGluAlaAlaGluProArg  200
Db  541 GACATCACGTGGATGAAGGACGACACCAGGCCTTGAGCGGCCGCTGAGCCCAGG  600

Qy  201 LysLysLysTrpThrLeuSerLeuLysAsnLeuArgProGluAspSerGlyLysTyrThr  220
Db  601 AAGAAGAAGTGGACACTGAGCCTGAAGAACCTGCGGCCGGAGGACAGCGGCAAATACACC  660

Qy  221 CysArgValSerAsnArgAlaGlyAlaIleAsnAlaThrLysTyrLysValAspValIleGln  240
Db  661 TGCCGGGTGTGCAACCGCGGGGCCATCAACGCCACTAAGTGGATGTGATCCAG  720

Qy  241 ArgThrArgSerLysProValLeuThrGlyThrHisProValAsnThrThrValAspPhe  260
Db  721 CGGACCCGTTCCAAGCCCGTGCTCACGGCACAGCCCGTGAACACGACGGTGGACTTC  780

Qy  261 GlyGlyThrThrSerPheGlnCysGlyValArgSerAspValLysProValIleGlnTrp  280
Db  781 GGGGGACCACCGTCCTTCCAGTGCAGGTGCGCAGGCGACGTGAAGCCGGTGATCCAGTGG  840

Qy  281 LeuLysArgValGluTyrGlyAlaGluGlyValArgHisAsnSerThrIleAspValGlyGly  300
Db  841 CTGAAGCGCGTGGAGTACGGCGCGGAGGGCGTGAGGCACAACTCCACCATCGATGTGGGCGGC  900

Qy  301 GlnLysPheValValLeuProThrGlyAspValTrpSerArgProAspGlySerTyrLeu  320
Db  901 CAGAAGTTTGTGGTGCTGCCCACGGGTGACGTGTGCTCGCGGCCCGACGGCTCCTACCTC  960

Qy  321 AsnLysLeuLeuIleThrArgAlaArgGlnAspAspAspAlaAlaArgGlyMetTyrIleCysLeuGly  340
Db  961 AATAAGCTGCTCATCACCCGTGCCCAGGACGATGCGGCATGTACATCTGCCTTGGC  1020

Qy  341 AlaAsnThrMetGlyTyrSerPheArgSerAlaPheLeuThrValLeuProAspAspProLys  360
Db 1021 GCCAACACCATGGCTACAGCTTCCGCAGCGCCTTCCTCACCGTGCTGCCAGACCCAAAA  1080

Qy  361 ProProGlyProProValAlaSerSerSerAlaThrSerLeuProTrpProValVal  380
Db 1081 CCGGCCAGGGCCACCTGTGGCCCTCCTGTCCTCGGCCCACTAGCCTGCCGTGGCCCGGGTC  1140

Qy  381 IleGlyIleProAlaGlyAlaValPheIleLeuValThrLeuLeuTrpLeuCysGln  400
Db 1141 ATCGGCATCCCAGCCGGCGCTGTCTTCATCCTGGGCACCCTGCTCTGGCTTTGCCAG  1200

Qy  401 AlaGlnLysLysProCysThrProAlaProLeuProGlyHisArgProPro  420
Db 1201 GCCCAGAAGAAGCCGTGCACCCCCGCCCCTGCCCCTGGGCACCGCCCGCCCG  1260

Qy  421 GlyThrAlaArgAspArgSerGlyAspLysProSerLeuAlaAlaLeuSerAla  440
Db 1261 GGGACGGCGCCGCGACCCGAGCGCGGAGACAAGGACCTTCCTCGTTGGCGCCCTCAGCGCT  1320

Qy  441 GlyProGlyValGlyLeuCysGluHisGlySerProAlaProGlnHisLeuLeu  460
Db 1321 GGCCCTGGTGTGGGGCTGTGTGAGGAGCATGGCTCTCCGGCAGCCACTTACTG  1380

Qy  461 GlyProGlyProValAlaGlyProLysLeuTyrProLysLeuTyrProLysAspIleHisThr  480
Db 1381 GGCCCAGGCCCAGTTGTGCCCTAAGTTGTACCCCAAACTCTACACAGACATCCACACA  1440

Qy  481 HisThrHisThrHisSerHisHisSerHisValGluValLysValHisGlnHisIle  500
Db 1441 CACACCACACCACTCTCACACACTCACACGTGGAGGCAAGGTCCACCAGCACATC  1500

Qy  501 HisTyrGlnCys  504
Db 1501 CACTATCAGTGC  1512
```

RESULT 2

Copyright   GenCore version 5.1.6
            Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 8, 2003, 16:29:18 ; Search time 3342.44 Seconds
                                             (without alignments)
                                             4381.722 Million cell updates/sec

Title: US-10-001-848-3_COPY_18_375
Perfect score: 1894
Sequence: 1 AFPPAAAARGPPKMADKVVP.........LPDPKPGPPVASSSSATSL 358

Scoring table: BLOSUM62
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               Ygapop 10.0 , Ygapext 0.5
               Fgapop 6.0 , Fgapext 7.0
               Delop   6.0 , Delext   7.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-D=GenEmbl -QFMT=fastp -SUFFIX=rge -MINMATCH=0.1 -LOOPCT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USR=US1001848_@CGN_1_4241@runat_08102003_130420_22053 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
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          3:   gb_in:*
          4:   gb_om:*
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          6:   gb_pat:*
          7:   gb_ph:*
          8:   gb_pl:*
          9:   gb_pr:*
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         11:   gb_sts:*
         12:   gb_sy:*
         13:   gb_un:*
         14:   gb_vi:*
         15:   em_ba:*
         16:   em_fun:*
         17:   em_hum:*
         18:   em_in:*
         19:   em_mu:*
         20:   em_om:*
         21:   em_or:*
         22:   em_ov:*
         23:   em_pat:*
         24:   em_ph:*
         25:   em_pl:*
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         27:   em_sts:*
         28:   em_un:*
         29:   em_vi:*
         30:   em_htg_hum:*
         31:   em_htg_inv:*
         32:   em_htg_other:*
         33:   em_htg_mus:*
         34:   em_htg_pln:*
         35:   em_htg_rod:*
         36:   em_htg_man:*
         37:   em_htg_vrt:*
         38:   em_sy:*
         39:   em_htgo_hum:*
         40:   em_htgo_mus:*
         41:   em_htgo_other:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1894	100.0	1450	6	AX287596	AX287596 Sequence
2	1894	100.0	3305	9	BC036769	BC036769 Homo sapi
3	1894	100.0	3402	6	AR252460	AR252460 Sequence
4	1894	100.0	3402	6	AX080803	AX080803 Sequence
5	1894	100.0	3402	6	AX191426	AX191426 Sequence
6	1894	100.0	3402	6	AX403231	AX403231 Sequence
7	1886	99.6	1565	9	AF279689	AF279689 Homo sapi
8	1886	99.6	3080	6	AX287610	AX287610 Sequence
9	1886	99.6	3080	9	HSA277437	AJ277437 Homo sapi
10	1886	99.6	3112	6	AX287608	AX287608 Sequence
11	1886	99.6	3397	9	AF312678	AF312678 Homo sapi
12	1785	94.2	1967	6	AR156834	AR156834 Sequence
13	1785	94.2	2274	10	MMU293947	AJ293947 Mus muscu
14	1785	94.2	2277	6	AX287593	AX287593 Sequence
15	1785	94.2	2359	10	AF321300	AF321300 Mus muscu
16	1767	93.3	1788	9	AX287613	AX287613 Sequence
17	1566	82.7	1004	6	AR156836	AR156836 Sequence
18	1468	77.5	177950	9	AC019103	AC019103 Homo sapi
19	1414.5	74.7	3256	10	AF321302	AF321302 Mus muscu
20	1410.5	74.5	24181	10	MMU308490	AJ308490 Mus muscu
21	1410.5	74.5	165443	2	AC079939	AC079939 Mus muscu
22	1410.5	74.5	176874	2	AC123743	AC123743 Mus muscu
23	1402.5	74.0	2774	5	BC053245	BC053245 Danio rer
24	1402.5	74.0	187234	2	AC117047	AC117047 Rattus no
25	1402.5	74.0	346077	2	AC106235	AC106235 Rattus no
26	1364	72.0	2178	6	AX224732	AX224732 Sequence
27	1356.5	71.6	232203	2	AC127933	AC127933 Rattus no
28	1290	68.1	2339	10	AF321301	AF321301 Mus muscu
29	1279.5	67.6	1742	6	AR156835	AR156835 Sequence
30	1164	61.5	781	6	AX080801	AX080801 Sequence
31	1154.5	61.0	182635	2	AC140291	AC140291 Mus muscu
32	861	45.5	493	6	AX318742	AX318742 Sequence
33	611	32.3	384	6	AR156833	AR156833 Sequence
34	606	32.0	152648	2	AC122772	AC122772 Mus muscu
35	524	27.7	148850	2	BX247870	BX247870 Mus muscu
36	524	27.7	204579	2	AL954843	AL954843 Danio rer
37	492	26.0	3002	5	AF157560	AF157560 Danio rer
38	487	25.7	3468	5	PWFGFR4	X65059 P.waltlii m
39	484.5	25.6	2763	5	PWFGFR3	X75603 P.waltlii m
40	482.5	25.5	3634	5	XLU24491	U24491 Xenopus lae
41	482.5	25.5	3815	5	XELX1FGFR	M55163 Xenopus lae
42	475.5	25.1	2520	10	S56291	S56291 sam3=FGFR3
43	475.5	25.1	4156	10	BC053056	BC053056 Mus muscu
44	475.5	25.1	4158	10	MUSMFR3	M81342 BALB/c fibr
45	473.5	25.0	2403	6	AX695736	AX695736 Sequence

ALIGNMENTS

RESULT 1

Qy 121 AspProAlaSerGlnGlnTrpAlaAlaArgGlyProArgPheThrGlnProSerLysMetArgArg 140
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Db 444 GACCCCGCCAGCCAGCAGTGGGCACGACCGCGGCTTCACCAGCCCTCCAAGATGAGGCGC 503

Qy 141 ArgValIleAlaArgProValGlySerSerValArgLeuLysCysValAlaSerGlyHis 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 504 CGGGTGATCGCACGGCCCGTGGTAGCTCCGTGCGGCTCAAGTGCGTGGCCAGCGGGCAC 563

Qy 161 ProArgProAspIleThrTrpMetLysAspAspGlnAlaLeuThrArgProGluAlaAla 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 564 CCTCGGCCCGACATCACGTGGATGAAGGACGACCAGGCCTTGACGCGGCCCAGAGGCCGCT 623

Qy 181 GluProArgGlyLysLysTrpThrLeuSerLeuLysAsnLeuArgProGluAspSerGlyIle 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 624 GAGCCCAGGAGAAGAAGTGGACACTGAGCCTGAAGAACCTGCGCCCGGAGACAGCGGC 683

Qy 201 LysTyrThrCysArgValSerArgAsnArgAlaGlyValAlaIleAsnAlaThrTyrLysValAsp 220
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 684 AAATACACCTGCCGCGTGTCGAACCGGGCGGGCCATCAACGCCACCTACAAGGTGGAT 743

Qy 221 ValIleGlnArgThrArgSerLysProValLeuThrGlyThrHisProValAsnThrThr 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 744 GTGATCCAGCGGCGGACCCGTTCCAAGCCCGTGCTCACAGGCACGCACCCCGTGAACACGACG 803

Qy 241 ValAspPheGlyGlyThrThrSerPheGlnCysLysValArgSerAspValLysProVal 260
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 804 GTGGACTTCGGGGGGACCACGTCCTTCCAGTGCAAGGTGCGCAGCGACGTGAAGCCGGTG 863

Qy 261 IleGlnTrpLeuLysArgValGluTyrGlyValGlyAlaGluGlyArgHisAsnSerThrIleAsp 280
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Db 864 ATCCAGTGGCTGAAGCGCGTGGAGTACGGCGTGGGTGAGGGGCGCCACAACTCCACCATCGAT 923

Qy 281 ValGlyGlyGlnLysPheValValLeuProThrGlyAspValTrpSerArgProAspAspGly 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 924 GTGGGCGGCCAGAAGTTTGTGGTGCTGCCCACGGGTGACGTGTGGTCGCGGCCCGACGGC 983

Qy 301 SerTyrLeuAsnLysLeuLeuIleThrArgAlaArgGlnAspAlaAspAlaGlyMetTyrIle 320
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 984 TCCTACCTCAATAAGCTGCTCATCACCCGTGCCCGCCAGGACGATGCGGACGCCATGTACATC 1043

Qy 321 CysLeuGlyAlaAsnThrMetGlyTyrSerPheArgSerAlaPheLeuThrValLeuPro 340
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1044 TGCCTTGGGCCCAACACCATGGGCTACAGCTTCCGCAGCGCCTTCCTCACCGTGCTGCCCA 1103

Qy 341 AspProLysProGlyProGlyProValAlaSerSerSerSerAlaThrSerLeu 358
         ||||||||||||||||||||||||||||||||||||||||||||||
Db 1104 GACCCCAAAACCGCCAGGGCCACCTGTGGCCTCCGTCCTCGGCCCACTAGCCTG 1:57

RESULT 2
BC036769
LOCUS   BC036769   3305 bp   mRNA   linear   PRI 26-AUG-2002
DEFINITION   Homo sapiens, clone MGC:46034 IMAGE:5744684, mRNA, complete cds.
ACCESSION   BC036769
VERSION   BC036769.1 GI:22477841
KEYWORDS   MGC.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 3305)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (23-AUG-2002) National Institutes of Health, Mammalian
             Gene Collection (MGC), Cancer Genomics Office, National Cancer
             Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
             USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: National Institutes of Health Intramural

---

AX287596
LOCUS   AX287596   1450 bp   DNA   linear   PAT 21-NOV-2001
DEFINITION   Sequence 4 from Patent WO0170977.
ACCESSION   AX287596
VERSION   AX287596.1 GI:17049361
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Saris,C.M., Mu,S.X., Xia,M., Boone,T.C. and Covey,T.
  TITLE   Fibroblast growth factor receptor-like molecules and uses thereof
  JOURNAL   Patent: WO 0170977-A 4 27-SEP-2001;
             Amgen, Inc. (US) ; Saris, Christiaan M. (US) ; Mu, Sharon X. (US) ;
             Xia, Min (US) ; Boone, Thomas Charles (US) ; Covey, Todd (US)
FEATURES   Location/Qualifiers
     source   1..1450
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     CDS   33..>1448
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD12303.1"
                     /db_xref="GI:17049362"
                     /translation="MTPSPLLLLLLPPLLGAFPPAAAARGPKMADKVVPRQVARLG
                     RTVRLQCPVBGDPPPLTMWTKDGRTIHSGWSRRFRVLPOGLKVKQVEREDAGVYVCKAT
                     NGFGSLSVNTLVVLDDISPGKESLGPDSSSGGOEDPASQQWARPRFTQPSKMRRRVI
                     ARPVGSSVRLKCVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPEDSGK
                     YTCRVSNRAGAINATYKVDVIQRTRSKPVLTGTHPVNTTVDFGGTTSFQCKVRSDVKP
                     VIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGDVWSRPDSGYLNKLLITRARQDDAG
                     MYICLGANTMGYSFRSAFLTVLPDPKPPGPPVASSSATSLPWPVVIGIPAGAVFILG
                     TLLLWLCQAQKKPCTPAPAPLPGHRPPGTARDRSGDKLPSLAALSAGPGVGLCEEH
                     GSPAAPQHLLGPGPVAGPKLYP"
     sig_peptide   33..104
BASE COUNT   243 a   516 c   480 g   211 t
ORIGIN

Alignment Scores:
Pred. No.:
Score: 1.57e-108   Length: 1450
Percent Similarity: 1894.00   Matches: 358
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 100.00%   Indels: 0
                         6   Gaps: 0

US-10-001-848-3_COPY_18_375 (1-358) x AX287596 (1-1450)

Qy   1 AlaPheProAlaAlaAlaAlaAlaArgGlyProProLysMetAlaAspLysValValPro 20
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Db 84 GCCTTCCCACCGGCCGCCGCCGGCGCCCCCAAAGATGGCGGACAAGGTGGTCCCCA 143

Qy 21 ArgGlnValAlaArgLeuGlyArgThrValArgLeuGlnCysProValGluGlyAspPro 40
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db 144 CGGCAGGTGGCCCGGCTGGGCCGCACTGTGCGGCTGCAGTGCCCAGTGGAGGGGGACCCG 203

Qy 41 ProProLeuThrMetTrpThrLysAspGlyArgThrIleHisSerGlyTrpSerArgPhe 60
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Db 204 CCGCCGCTGACCATGTGGACCAAGGATGGCCGCACCATCCACAGCGGCTGGAGCCGCTTC 263

Qy 61 ArgValLeuProGlnGlyLeuLysValLysGlnValGluArgGluAspAlaGlyValTyr 80
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Db 264 CGCGTGCTGCCGCAGGGCCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCCGGCGTGTAC 323

Qy 81 ValCysLysAlaThrAsnGlyPheGlySerLeuSerValAsnThrLeuValValLeu 100
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Db 324 GTGTGCAAGGCCACCAACGGCTTCGGCAGCCTGAGCGTCAACACCCTCGTCGTGCTG 383

Qy 101 AspAspIleSerProGlyLysGluSerLeuGlyProAspSerSerSerGlyGlyGlnGlu 120
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Db   3. GATGACATTAGCCCAGGGAAGGAGAGCCTGGGGCCCCGACAGCTCCTCTGGGGGTCAGAG 443

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Db  301 QKFVVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVLPDPK 360
Qy  361 PPGPPVASSSSATSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPP 420
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Db  361 PPGPPVASSSSATSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPP 420
Qy  421 GTARDRSGDKDLPSLAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHT 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GTARDRSGDKDLPSLAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHT 480
Qy  481 HTHTHSHTHSHVBGKVHQHIHYQC 504
        |||||||||||| |||||||||||
Db  481 HTHTHSHTHSHVEGKVHQHIHYQC 504
```

RESULT 7
AAU81961
ID   AAU81961 standard; Protein; 504 AA.
XX
AC   AAU81961;
XX
DT   09-APR-2002 (first entry)
XX
DE   Human PRO943.
XX
KW   Human; PRO; antiinflammatory; ophthalmological; vasotropic;
KW   retinal cell injury; ocular disease; retinitis pigmentosa;
KW   macular degeneration; retinal detachment; retinal tear; retinopathy;
KW   retinal degenerative disease; macular hole; degenerative myopia;
KW   acute retinal necrosis syndrome; oedema; ischaemic condition;
KW   Purtscher's retinopathy; oedema; collagen vascular disease;
KW   retinal vision occlusion; collagen vascular disease;
KW   thrombocytopaenic purpura; uveitis; retinal vasculitis;Eales disease;
KW   systemic lupus erythematosus; environmental trauma.
XX
OS   Homo sapiens.
XX
PN   WO200109327-A2.
XX
PD   08-FEB-2001.
XX
PF   28-JUL-2000; 2000WO-US20710.
XX
PR   28-JUL-1999; 99US-146222P.
PR   13-SEP-1999; 99WO-US20944.
PR   15-SEP-1999; 99WO-US21090.
PR   29-NOV-1999; 99WO-US28214.
PR   30-NOV-1999; 99WO-US28313.
PR   01-DEC-1999; 99WO-US28301.
PR   05-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   22-FEB-2000; 2000WO-US04414.
PR   24-FEB-2000; 2000WO-US05004.
PR   02-MAR-2000; 2000WO-US05841.
PR   15-MAR-2000; 2000WO-US06884.
PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;
PI   Kljavin IJ, Lafleur M, Mark MR, Marsters SA, Pitti RM;
PI   Watanabe CK, Wood WI;
XX
DR   WPI: 2002-130120/17.
DR   N-PSDB; ABK28591.
XX
PT   Promoting survival of retinal cells, or delaying or preventing retinal
PT   cell injury or death, by contacting retinal cells with PRO175, 220,
PT   216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132
PT   polypeptide -

XX
PS   Claim 44; Fig 19; 152pp; English.
XX
CC   The invention relates to promoting the survival of retinal cells, or
CC   delaying or preventing retinal cell injury or death, by contacting the
CC   retinal cells with the polypeptide such as PRO175, PRO220, PRO216,
CC   PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO826,
CC   PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids
CC   encoding the PRO proteins, a vector comprising the nucleic acid, a host
CC   cell comprising the vector, and anti-PRO antibody. The PRO proteins are
CC   useful for promoting survival of retinal cells (retinal neurons such as
CC   retinal ganglion cells, displaced retinal ganglion cells, amacrine
CC   cells, displaced amacrine cells, horizontal neurons or bipolar neurons,
CC   rod photoreceptors, or supportive cells such as Muller cells or pigment
CC   epithelial cells), or delaying or preventing retinal cell injury or
CC   death caused by ocular disease (which is or is associated with
CC   retinitis pigmentosa, macular degeneration, retinal detachment, ret
CC   tear, retinopathy, retinal degenerative disease, macular hole,
CC   degenerative myopia, acute retinal necrosis syndrome, traumatic
CC   chorioretinopathy or contusion, Purtscher's retinopathy, oedema, a
CC   ischaemic condition, central or branch retinal vision occlusion, retinal
CC   collagen vascular disease, thrombocytopaenic purpura, uveitis, retinal
CC   vasculitis, occlusion associated with Eales disease or systemic lupus
CC   erythematosus), retinal injury or death is delayed or prevented by substantially not
CC   cell injury or death is delayed or prevented by substantially not
CC   causing angiogenesis or mitogenesis. The present sequence represents
CC   a PRO protein.
XX
SQ   Sequence   504 AA;

Query Match   100.0%; Score 2709; DB 23; Length 504;
Best Local Similarity   100.0%; Pred. No. 7.3e-164;
Matches 504; Conservative   0; Mismatches   0; Indels 0; Gaps 0;

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Db    1 MTPSPLLLLLPPLLGAFFPPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPL 60

Qy   61 TMWTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYYCKATNGFGSLSVNYTLVVLDDI 120
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Db   61 TMWTKDGRTIHSGWSRFRVLPQGLKVKQVERBDAGVYVCKATNGFGSLSVNYTLVVLDDI 120

Qy  121 SPGKESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRP 180
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Db  121 SPGKESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRP 180

Qy  181 DITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQ 240
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Db  181 DITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPBDSGKYTCRVSNRAGAINATYKVDVIQ 240

Qy  241 RTRSKPVLTGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGABGRHNSTIDVGG 300
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Db  241 RTRSKPVLTGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGG 300

Qy  301 QKFVVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVLPDPK 360
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Db  301 QKFVVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVLPDPK 360

Qy  361 PPGPPVASSSSATSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPP 420
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Db  361 PPGPPVASSSSATSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPP 420

Qy  421 GTARDRSGDKDLPSLAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHT 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GTARDRSGDKDLPSLAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHT 480

Qy  481 HTHTHSHTHSHVEGKVHQHIHYQC 504
        ||||||||||||||||||||||||
Db  481 HTHTHSHTHSHVEGKVHQHIHYQC 504
```

RESULT 8
ABU59072

ID   ABU59072 standard; Protein; 504 AA.
XX
AC   ABU59072;
XX
DT   28-APR-2003 (first entry)
XX
DE   Novel human secreted or transmembrane protein PRO943.
XX
KW   Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW   cardiac insufficiency disorder; cancer; tumour; immune response;
KW   adrenal cortical capillary endothelial growth; c-fos induction;
KW   vascular endothelial growth factor inhibition; VEGF inhibition;
KW   endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW   retinal neurons cell survival; rod photoreceptor cell survival;
KW   retinal disorder; retinitis pigmentosum; kidney disorder;
KW   mammalian kidney mesangial cell proliferation; Berger disease;
KW   dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;
KW   chondrocyte redifferentiation; sports injury; arthritis.
XX
OS   Homo sapiens
XX
PN   US2002132252-A1.
XX
PD   19-SEP-2002.
XX
PF   14-NOV-2001; 2001US-0990442.
XX
PR   05-NOV-1997; 97WO-US20069.
PR   16-SEP-1998; 98WO-US19330.
PR   17-SEP-1998; 98WO-US19437.
PR   07-OCT-1998; 98WO-US21141.
PR   01-DEC-1998; 98WO-US25108.
PR   05-JAN-1999; 99WO-US00106.
PR   08-MAR-1999; 99WO-US05028.
PR   02-JUN-1999; 99WO-US12252.
PR   15-SEP-1999; 99WO-US21090.
PR   15-SEP-1999; 99WO-US21547.
PR   30-NOV-1999; 99WO-US28813.
PR   01-DEC-1999; 99WO-US28301.
PR   01-DEC-1999; 99WO-US28634.
PR   16-DEC-1999; 99WO-US30095.
PR   20-DEC-1999; 99WO-US30911.
PR   06-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   22-FEB-2000; 2000WO-US04414.
PR   24-FEB-2000; 2000WO-US04914.
PR   24-FEB-2000; 2000WO-US05004.
PR   02-MAR-2000; 2000WO-US05841.
PR   02-MAR-2000; 2000WO-US06319.
PR   15-MAR-2000; 2000WO-US06884.
PR   20-MAR-2000; 2000WO-US07377.
PR   20-MAR-2000; 2000WO-US08439.
PR   15-MAY-2000; 2000WO-US13358.
PR   17-MAY-2000; 2000WO-US13705.
PR   24-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   28-JUL-2000; 2000WO-US20710.
PR   11-AUG-2000; 2000WO-US22031.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   08-NOV-2000; 2000WO-US30952.
PR   01-DEC-2000; 2000WO-US32678.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-JUN-2001; 2001WO-US17800.
PR   20-JUN-2001; 2001WO-US19692.
PR   29-JUN-2001; 2001WO-US21066.
PR   09-JUL-2001; 2001WO-US21735.
PR   16-JUN-1997; 97US-049787P.
PR   17-OCT-1997; 97US-062250P.
PR   12-NOV-1997; 97US-065186P.

PR   13-NOV-1997; 97US-065311P.
PR   24-NOV-1997; 97US-066770P.
PR   25-FEB-1998; 98US-075945P.
PR   20-MAR-1998; 98US-078910P.
PR   28-APR-1998; 98US-083322P.
PR   07-MAY-1998; 98US-084600P.
PR   28-MAY-1998; 98US-087106P.
PR   02-JUN-1998; 98US-087607P.
PR   02-JUN-1998; 98US-087609P.
PR   02-JUN-1998; 98US-087759P.
PR   03-JUN-1998; 98US-087827P.
PR   04-JUN-1998; 98US-088021P.
PR   04-JUN-1998; 98US-088025P.
PR   04-JUN-1998; 98US-088026P.
PR   04-JUN-1998; 98US-088028P.
PR   04-JUN-1998; 98US-088029P.
PR   04-JUN-1998; 98US-088030P.
PR   04-JUN-1998; 98US-088033P.
PR   04-JUN-1998; 98US-088326P.
PR   05-JUN-1998; 98US-088167P.
PR   05-JUN-1998; 98US-088202P.
PR   05-JUN-1998; 98US-088212P.
PR   05-JUN-1998; 98US-088217P.
PR   09-JUN-1998; 98US-088655P.
PR   10-JUN-1998; 98US-088734P.
PR   10-JUN-1998; 98US-088738P.
PR   10-JUN-1998; 98US-088742P.
PR   10-JUN-1998; 98US-088881CP.
PR   10-JUN-1998; 98US-088824P.
PR   10-JUN-1998; 98US-088826P.
PR   11-JUN-1998; 98US-088858P.
PR   11-JUN-1998; 98US-088861P.
PR   11-JUN-1998; 98US-088876P.
PR   12-JUN-1998; 98US-089105P.
PR   16-JUN-1998; 98US-089440P.
PR   16-JUN-1998; 98US-089512P.
PR   16-JUN-1998; 98US-089514P.
PR   17-JUN-1998; 98US-089532P.
PR   17-JUN-1998; 98US-089538P.
PR   17-JUN-1998; 98US-089598P.
PR   17-JUN-1998; 98US-089599P.
PR   17-JUN-1998; 98US-089600P.
PR   17-JUN-1998; 98US-089653P.
PR   18-JUN-1998; 98US-089801P.
PR   18-JUN-1998; 98US-089907P.
PR   18-JUN-1998; 98US-089908P.
PR   28-AUG-2001; 2001US-0941992
XX
PA   (GETH) GENENTECH INC.
XX
PI   Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI   Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI   Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI   Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI   Zhang Z;
XX
DR   WPI; 2003-247083/24.
DR   N-PSDB; ABX80197.
XX
PT   Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT   and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT   are therapeutically useful for enhancing immune response and in cancer
PT   treatments -
XX
PS   Claim 12; Fig 70; 648pp; English.
XX
CC   The invention describes an isolated human PRO polypeptide. The PRO
CC   polypeptides are useful in detecting PRO polypeptides in a sample, in
CC   linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC   in modulating at least one biological activity of a cell expressing a PRO
CC   polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC   useful for treating cardiac insufficiency disorders. PRO154 and PRO1186
CC   stimulate adrenal cortical capillary endothelial growth, and PRO536,